

#2 OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/003,356

DATE: 12/13/2001  
TIME: 09:00:36

Input Set : A:\00-107.SEQ.txt  
Output Set: N:\CRF3\12132001\I003356.raw

4 <110> APPLICANT: Lok, Si  
5 Holloway, James L.  
7 <120> TITLE OF INVENTION: Human V2 Vomeronasal Receptor  
9 <130> FILE REFERENCE: 00-107  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/003,356  
C--> 11 <141> CURRENT FILING DATE: 2001-11-15  
11 <150> PRIOR APPLICATION NUMBER: 60/252,373  
12 <151> PRIOR FILING DATE: 2000-11-21  
14 <160> NUMBER OF SEQ ID NOS: 10  
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 657  
20 <212> TYPE: DNA  
21 <213> ORGANISM: HOMO sapiens  
23 <220> FEATURE:  
24 <221> NAME/KEY: CDS  
25 <222> LOCATION: (1)...(657)  
27 <400> SEQUENCE: 1  
28 atg ttt gag agg cgc aaa gag caa gac gag gga cca gga atc cat gaa 48  
29 Met Phe Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu  
30 1 5 10 15  
32 ttt ctt gca ttt tta tgg gct gaa ttg ggc tct gaa gcc aaa gaa gag 96  
33 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu  
34 20 25 30  
36 aaa gaa gaa gaa cgg acc tgc cgg ttg ctg ggc aag tgt gta gat gcc 144  
37 Lys Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala  
38 35 40 45  
40 gaa aac cat tcc ctt gtt att gga gga ctg ttt cct att gac tcc agg 192  
41 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg  
42 50 55 60  
44 acc atc cca gca aat gag tct att ttg gag cca gca tca gca aaa tgt 240  
45 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys  
46 65 70 75 80  
48 gaa ggg ttt aac ttt cag aga ttc cgc tgg atg aaa gcc atg atc cac 288  
49 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His  
50 85 90 95  
52 atg atc aag gag att aat aag agg aag gat att ttg ccc aac atc act 336  
53 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr  
54 100 105 110  
56 ctg ggc tat cag atc ttt gat acc tgt ttt acc atc tcc aaa tca gtg 384  
57 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val  
58 115 120 125  
60 gaa gca gtc ttg gta ttt ctt aca ggg cag gaa gaa aac agg ccc aat 432  
61 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn  
62 130 135 140  
64 ttt aga aac agc act gga gca ttt ccg gca gga att gtt gga gca ggt 480  
65 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly

ENTERED

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```

66 145           150           155           160
68 gga tca ttc tta tca gtt cct gct tca aga att cta ggg tta tat tat 528
69 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
70           165           170           175
72 ttg cct cag gtg ggc tat acc tct acc tgc gtg att ctt agt gac aaa 576
73 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
74           180           185           190
76 tac cag ttt cca tct tat ctt cgt gta ata gcc agc gat aag atc cag 624
77 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
78           195           200           205
80 tcg aag gct gtg gta aaa cgt atc caa cac ttt
81 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
82           210           215
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 219
86 <212> TYPE: PRT
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 2
90 Met Phe Glu Arg Arg Lys Glu Gln Asp Glu Gly Pro Gly Ile His Glu
91   1           5           10           15
92 Phe Leu Ala Phe Leu Trp Ala Glu Leu Gly Ser Glu Ala Lys Glu Glu
93   20          25          30
94 Lys Glu Glu Glu Arg Thr Cys Arg Leu Leu Gly Lys Cys Val Asp Ala
95   35          40          45
96 Glu Asn His Ser Leu Val Ile Gly Gly Leu Phe Pro Ile Asp Ser Arg
97   50          55          60
98 Thr Ile Pro Ala Asn Glu Ser Ile Leu Glu Pro Ala Ser Ala Lys Cys
99  65           70           75           80
100 Glu Gly Phe Asn Phe Gln Arg Phe Arg Trp Met Lys Ala Met Ile His
101    85          90          95
102 Met Ile Lys Glu Ile Asn Lys Arg Lys Asp Ile Leu Pro Asn Ile Thr
103    100         105         110
104 Leu Gly Tyr Gln Ile Phe Asp Thr Cys Phe Thr Ile Ser Lys Ser Val
105    115         120         125
106 Glu Ala Val Leu Val Phe Leu Thr Gly Gln Glu Glu Asn Arg Pro Asn
107    130         135         140
108 Phe Arg Asn Ser Thr Gly Ala Phe Pro Ala Gly Ile Val Gly Ala Gly
109  145          150          155          160
110 Gly Ser Phe Leu Ser Val Pro Ala Ser Arg Ile Leu Gly Leu Tyr Tyr
111    165         170         175
112 Leu Pro Gln Val Gly Tyr Thr Ser Thr Cys Val Ile Leu Ser Asp Lys
113    180         185         190
114 Tyr Gln Phe Pro Ser Tyr Leu Arg Val Ile Ala Ser Asp Lys Ile Gln
115    195         200         205
116 Ser Lys Ala Val Val Lys Arg Ile Gln His Phe
117    210         215
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 657
121 <212> TYPE: DNA

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122 <213> ORGANISM: Artificial Sequence  
 124 <220> FEATURE:  
 125 <223> OTHER INFORMATION: This degenerate nucleotide sequence encodes the  
 126 amino acid sequence of SEQ ID NO:2.  
 128 <221> NAME/KEY: misc\_feature  
 129 <222> LOCATION: 12, 15, 33, 36, 39, 54, 57, 63, 69, 75, 78, 81, 87, 111,  
 130 114, 120, 123, 126, 129, 138, 144, 156, 159, 162, 168, 171,  
 131 174, 180, 189, 192, 195, 201, 204, 213, 219, 225, 228, 231,  
 132 234, 246, 261, 267, 279, 312, 324, 327, 336, 339, 342  
 133 <223> OTHER INFORMATION: n = A,T,C or G  
 135 <221> NAME/KEY: misc\_feature  
 136 <222> LOCATION: 360, 369, 375, 381, 384, 390, 393, 396, 399, 405, 408, 411,  
 137 426, 429, 438, 444, 447, 450, 453, 459, 462, 465, 471, 474,  
 138 477, 480, 483, 486, 492, 495, 498, 501, 504, 507, 510, 516,  
 139 519, 522, 531, 534, 540, 543, 549, 552, 555, 561, 567  
 140 <223> OTHER INFORMATION: n = A,T,C or G  
 142 <221> NAME/KEY: misc\_feature  
 143 <222> LOCATION: 570, 588, 591, 597, 600, 603, 609, 612, 627, 633, 636, 639,  
 144 645  
 145 <223> OTHER INFORMATION: n = A,T,C or G  
 147 <400> SEQUENCE: 3  
 W--> 148 atgtygarm gnmnaarga rcargaygar ggnccngna thcaygartt yytngcnatty 60  
 W--> 149 ytntggcng arytnnnws ngargcnaar gargaarg argargarmg nacntgymgn 120  
 W--> 150 ytnytngna artgygtnga ygcngaraay caywsnytng tnathggngg nytnnttyccn 180  
 W--> 151 athgaywsnm gnacnathcc ngcnaaygar wsnathytn arccngcnws ngcnaartgy 240  
 W--> 152 garggnttya ayttycarmg ntymgntgg atgaargcna tgathcayat gathaargar 300  
 W--> 153 athaayaarm gnaargayat hytnccnaay athacnytng gntaycarat httygayacn 360  
 W--> 154 tgyttaacna thwsnaarws ngtngargcn gtntgntnt tyytnacngg ncargargar 420  
 W--> 155 aaymgncna ayttymgnna ywsnacnngn gcnttccng cnngnathgt nngngcnngn 480  
 W--> 156 ggnwsnttlyy tnwsngtncc ngcnwsnmgn athytnngny ntaytayyt nccncargtn 540  
 W--> 157 ggntayacnw snacntgygt nathytnwsn gayaartayc arttycnws ntayytnmgn 600  
 W--> 158 gtnathgcnw sngayaarat hcarwsnaar gcngtngtna armgnathca rcaytta 657  
 160 <210> SEQ ID NO: 4  
 161 <211> LENGTH: 1140  
 162 <212> TYPE: DNA  
 163 <213> ORGANISM: Homo sapiens  
 165 <220> FEATURE:  
 166 <221> NAME/KEY: CDS  
 167 <222> LOCATION: (1)...(1140)  
 169 <400> SEQUENCE: 4  
 170 ctt ccc cat tca gtg tgt act gat gtg tgt cct cct ggg act gga agg 48  
 171 Leu Pro His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Gly Arg  
 172 1 5 10 15  
 174 gga ttc gtt cag agg gaa cca ata tgc tgc ttt gac tcc atc cca tgt 96  
 175 Gly Phe Val Gln Arg Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys  
 176 20 25 30  
 178 gct gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa 144  
 179 Ala Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln  
 180 35 40 45

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**Output Set: N:\CRF3\12132001\I003356.raw**

182	tgt ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg	192
183	Cys Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu	
184	50 55 60	
186	aaa gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt	240
187	Lys Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu	
188	65 70 75 80	
190	gtc att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct	288
191	Val Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala	
192	85 90 95	
194	gtg tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg	336
195	Val Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp	
196	100 105 110	
198	cag ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tcg	384
199	Gln Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser	
200	115 120 125	
202	tcc atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc	432
203	Ser Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly	
204	130 135 140	
206	cag gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt	480
207	Gln Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu	
208	145 150 155 160	
210	gga aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa	528
211	Gly Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys	
212	165 170 175	
214	act caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta	576
217	Thr Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu	
218	180 185 190	
220	atc tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg	624
221	Ile Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu	
222	195 200 205	
224	gaa cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc	672
225	Glu Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile	
226	210 215 220	
228	att ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt	720
229	Ile Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe	
230	225 230 235 240	
232	gga att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg	768
233	Gly Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val	
234	245 250 255	
236	gct cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt	816
237	Ala Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe	
238	260 265 270	
240	ggg atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat	864
241	Gly Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr	
242	275 280 285	
244	ttg agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc	912
245	Leu Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile	
246	290 295 300	
248	ttg gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc	960

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249	Leu	Ala	Ser	Ser	His	Gly	Leu	Leu	Gly	Cys	Ile	Phe	Ala	Pro	Lys	Cys
250	305					310			315							320
252	ctc	att	att	ttg	ctg	agg	cca	gag	agg	aac	acc	agt	gaa	att	gtt	tgt
253	Leu	Ile	Ile	Leu	Leu	Arg	Pro	Glu	Arg	Asn	Thr	Ser	Glu	Ile	Val	Cys
254						325			330							335
256	gga	aga	gtc	tcc	acc	aca	gat	aat	tgc	atc	caa	ctg	acc	tca	gct	ttt
257	Gly	Arg	Val	Ser	Thr	Thr	Asp	Asn	Cys	Ile	Gln	Leu	Thr	Ser	Ala	Phe
258						340			345							350
260	gtg	agc	agt	gag	ctt	aac	aat	acc	aca	gtg	tca	act	gtt	ctg	gat	gac
261	Val	Ser	Ser	Glu	Leu	Asn	Asn	Thr	Thr	Val	Ser	Thr	Val	Leu	Asp	Asp
262						355			360							365
264	aga	gtt	ttg	att	tac	atg	tgt	cct	ttg	aag	ctg	caa				1140
265	Arg	Val	Leu	Ile	Tyr	Met	Cys	Pro	Leu	Lys	Leu	Gln				
266						370			375							380
268	<210>	SEQ	ID	NO:	5											
269	<211>	LENGTH:	380													
270	<212>	TYPE:	PRT													
271	<213>	ORGANISM:	Homo sapiens													
273	<400>	SEQUENCE:	5													
274	Leu	Pro	His	Ser	Val	Cys	Thr	Asp	Val	Cys	Pro	Pro	Gly	Thr	Gly	Arg
275	1				5				10							15
276	Gly	Phe	Val	Gln	Arg	Glu	Pro	Ile	Cys	Cys	Phe	Asp	Ser	Ile	Pro	Cys
277						20			25							30
278	Ala	Asp	Gly	His	Val	Ser	Arg	Lys	Pro	Gly	Glu	Arg	Glu	Cys	Glu	Gln
279						35			40							45
280	Cys	Gly	Glu	Asp	Tyr	Trp	Ser	Asn	Ala	Gln	Lys	Ser	Glu	Cys	Val	Leu
281						50			55							60
282	Lys	Glu	Val	Glu	Tyr	Leu	Ala	Tyr	Asp	Glu	Ala	Leu	Gly	Phe	Thr	Leu
283						65			70							80
284	Val	Ile	Leu	Ser	Val	Phe	Gly	Ala	Phe	Val	Val	Leu	Ala	Val	Thr	Ala
285						85			90							95
286	Val	Tyr	Val	Ile	His	Arg	His	Thr	Pro	Leu	Val	Asn	Ala	Ser	Asp	Trp
287						100			105							110
288	Gln	Leu	Gly	Phe	Leu	Ile	Gln	Val	Ser	Leu	Ile	Ile	Met	Leu	Leu	Ser
289						115			120							125
290	Ser	Met	Leu	Phe	Ile	Asp	Lys	Pro	His	Asn	Trp	Ser	Cys	Met	Ala	Gly
291						130			135							140
292	Gln	Val	Thr	Leu	Ala	Leu	Gly	Phe	Ser	Leu	Cys	Leu	Ser	Cys	Leu	Leu
293						145			150							160
294	Gly	Lys	Thr	Ser	Ser	Leu	Phe	Leu	Ala	Tyr	Arg	Ile	Ser	Lys	Ser	Lys
295						165			170							175
296	Thr	Gln	Leu	Thr	Ser	Met	His	Pro	Leu	Tyr	Arg	Lys	Ile	Ile	Val	Leu
297						180			185							190
298	Ile	Ser	Val	Leu	Ala	Glu	Ile	Gly	Ile	Cys	Thr	Ala	Tyr	Leu	Ile	Leu
299						195			200							205
300	Glu	Pro	Pro	Met	Val	Tyr	Lys	Asn	Met	Glu	Ser	Gln	Asn	Thr	Lys	Ile
301						210			215							220
302	Ile	Leu	Gly	Cys	Asn	Glu	Ile	Ser	Ile	Glu	Phe	Leu	Tyr	Ser	Met	Phe
303						225			230							240

→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
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Input Set : A:\00-107.SEQ.txt  
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:149 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:151 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:155 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:366 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:383 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9